

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 20:21:08 ; Search time 169.55 Seconds  
(without alignments)  
556.212 Million cell updates/sec

Title: US-09-486-094-1

Perfect score: 110

Sequence: 1 aggtccgtgtgcaggcagat.....gaacgtgtgcagcgtccgg 110

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_1101.\*  
1: /SIDS1/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
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4: /SIDS1/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDS1/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDS1/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDS1/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
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13: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SIDS1/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SIDS1/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDS1/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	100.0	110	20	AA29727 Scorpion androcton
2	110	100.0	211	20	AA29729 Chimeric signal pe
3	97	88.2	97	20	AA29733 Oligo #4 for scorp
4	44	40.0	44	20	AA29732 cDNA encoding the
5	35	31.8	98	20	AA29772 DNA encoding a hel
6	34	30.9	169	21	AA245692 DNA encoding a fus
7	34	30.9	261	21	AA245693 cDNA encoding a th
8	33	30.0	197	20	AA259774 Hereditary haemoch
9	30.2	27.5	235033	19	AAV57926 Adenovirus 17. Ma
10	30.2	27.5	237326	19	AAV57903
11	28.4	25.8	35099	19	AAV27112

c 12	27.4	24.9	5362	18	AA297296	Mouse additional s
c 13	27.4	24.9	5362	18	AA297294	Mouse additional s
c 14	27.2	24.7	193	22	AA124592	Probe #14525 for g
c 15	27.2	24.7	193	22	AA149861	Probe #18547 used
c 16	27.2	24.7	393	22	AA297558	Novel human polynu
c 17	27.2	24.7	405	22	AA116146	Probe #6079 for ge
c 18	27.2	24.7	405	22	AA138435	Probe #7121 used t
c 19	27	24.5	6536	21	AA275801	Human OREF ORF1356
c 20	26.8	24.4	517	22	AA124525	Probe #14458 for g
c 21	26.8	24.4	1920	22	AA14309	Human cDNA sequenc
c 22	26.4	24.0	4650	22	AAH17670	Human cDNA sequenc
c 23	26.2	23.8	758	22	AAH05645	Human cDNA clone (
c 24	26.2	23.8	1572	22	AAH11694	Human odorant rece
c 25	26.2	23.8	1573	22	AAQ58553	Human p55Nuc. Hom
c 26	26.2	23.8	2297	22	AAH05087	Human secreted pro
c 27	26	23.6	391	21	AAH30679	Human colon cancer
c 28	26	23.6	2011	22	AAH14988	Human cDNA sequenc
c 29	26	23.6	2240	21	AAH08027	Human ENT1 recepto
c 30	26	23.6	2243	21	AAH37045	Human PRO1380 (UNQ
c 31	26	23.6	2243	22	AA294256	DNA encoding prote
c 32	26	23.6	2471	14	AAQ39041	Beta-tyrosinase ge
c 33	25.6	23.3	1470	21	AA278035	Human cancer assoc
c 34	25.6	23.3	3331	22	AA222442	Human cDNA encodin
c 35	25.6	23.3	3690	22	AA222678	Human cDNA encodin
c 36	25.6	23.3	5003	21	AA277125	Human OREF ORF2680
c 37	25.6	23.3	6481	22	AA159183	Human polynucleoti
c 38	25.6	23.3	10625	22	AA285836	Nucleotide sequenc
c 39	25.4	23.1	318	20	AAH11144	Human secreted pro
c 40	25.4	23.1	1152	22	AA288150	Human DNAX cytokin
c 41	25.4	23.1	4628	22	AA159328	Human polynucleoti
c 42	25.4	23.1	5714	22	AA260867	Human TAA R11 cDNA
c 43	25.2	22.9	1083	21	AA262728	Endoglucanase nucl
c 44	25	22.7	662	21	AA211078	Fusarium venenatum
c 45	25	22.7	2921	22	AAH16003	Human cDNA sequenc

#### ALIGNMENTS

#### RESULT 1

AA29727  
ID AA29727 standard; DNA; 110 BP.  
AC AA29727;  
XX  
XX  
DT 22-JUN-1999 (first entry)  
DE Scorpion androctonin toxin coding sequence.  
XX  
XX Toxin; androctonin; scorpion; fusion protein; transgenic plant;  
XX resistance; fungus; bacterium; infection; ss.  
XX Androctonus australis.  
XX  
XX WO9909189-A1.  
XX  
XX 25-FEB-1999.  
XX  
XX 18-AUG-1998; 98WO-FR01814.  
XX  
XX 20-AUG-1997; 97FR-0010632.  
XX  
XX (RHON ) RHONE-POULENC AGROCHIMIE.  
XX  
XX Derose R, Freyssinet G, Hoffmann J;  
XX  
XX WPI; 1999-181046/15.  
XX P-PSDB; AAW99575.  
XX  
XX DNA encoding scorpion peptide androctonin - especially for producing  
XX disease-resistant plants  
XX  
XX Claim 9; Page 25; 37pp; French.

```

XX
CC This sequence corresponds to the coding sequence for the toxin
CC androctonin from the scorpion Androctonus australis. The sequence
CC is used to generate a fusion gene for expression in a plant.
CC Transgenic plants containing androctonin genes are stated to be
CC resistant to fungal and bacterial infections, especially caused
CC by Cercospora beticola, Cladosporium herbarum, Fusarium culmorum,
CC Fusarium graminearum or Phytophthora cinnamomi.
XX
SQ Sequence 110 BP; 26 A; 25 C; 40 G; 19 T; 0 Other;

Query Match      100.0%; Score 110; DB 20; Length 110;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aggtcgtgtgcaggcagatcaagatctgcaggaggagggtgtgtgtctactacaagtgc 60
   |||||||
Db 1 aggtcgtgtgcaggcagatcaagatctgcaggaggagggtgtgtgtctactacaagtgc 60
   |||||||

QY 61 actaacagccatactagctgcaggcagcgaacgtgtcagcgatccgg 110
   |||||||
Db 61 actaacagccatactagctgcaggcagcgaacgtgtcagcgatccgg 110
   |||||||

RESULT 2
AAAX29729
ID AAX29729 standard; DNA; 211 BP.
XX
XX AAX29729;
XX
XX 22-JUN-1999 (first entry)
XX
XX Chimeric signal peptide toxin gene.
XX
XX Toxin; androctonin; scorpion; fusion protein; transgenic plant;
XX resistance; fungus; bacterium; infection; ss.
XX
XX Chimeric - Androctonus australis.
XX Chimeric - Nicotiana sp.
XX
XX W09909189-A1.
XX
XX 25-FEB-1999.
XX
XX 18-AUG-1998; 98WO-FR01814.
XX
XX 20-AUG-1997; 97FR-0010632.
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Derose R, Freyssinet G, Hoffmann J;
XX
XX WPI: 1999-181046/15.
XX P-PSDB; W.
XX
XX DNA encoding scorpion peptide androctonin - especially for producing
XX disease-resistant plants
XX
XX Claim 17; Page 26; 37pp; French.
XX
XX This sequence corresponds to the coding sequence for a fusion gene
XX comprising the tobacco PR-1alpha gene signal peptide sequence linked
XX to the gene encoding the toxin androctonin from the scorpion Androctonus
XX australis for expression in plants. Transgenic plants containing
XX androctonin genes are stated to be resistant to fungal and bacterial
XX infections, especially caused by Cercospora beticola, Cladosporium
XX herbarum, Fusarium culmorum, Fusarium graminearum or Phytophthora
XX cinnamomi.
XX
XX Sequence 211 BP; 33 A; 58 C; 57 G; 63 T; 0 Other;
SQ

```

AAAX29732  
ID AAX29732 standard; DNA; 44 BP.  
AC AAX29732;  
XX  
DT 22-JUN-1999 (first entry)  
XX  
DE Oligo #3 for scorpion toxin fusion gene.  
XX  
KW Toxin; androctonin; scorpion; fusion protein; transgenic plant;  
KW resistance; fungus; bacterium; infection; ss.  
XX  
OS Synthetic.  
XX  
PN WO9909189-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 18-AUG-1998; 98WO-FR01814.  
XX  
PR 20-AUG-1997; 97FR-0010632.  
XX  
PA (RHON ) RHONE-POULENC AGROCHIMIE.  
XX  
PI Derose R, Freyssinet G, Hoffmann J;  
XX  
DR WPI; 1999-181046/15.  
XX  
PT DNA encoding scorpion peptide androctonin - especially for producing  
XX disease-resistant plants  
XX  
PS Example 1; Page 12; 37pp; French.  
XX  
CC This sequence corresponds to an oligonucleotide used to generate a  
CC fusion gene (AAAX29729) comprising the tobacco PR-1alpha gene signal  
CC peptide sequence linked to the gene encoding the toxin androctonin  
CC from the scorpion Androctonus australis, for expression in plants.  
CC Transgenic plants containing androctonin genes are stated to be  
CC resistant to fungal and bacterial infections, especially caused by  
CC Cercospora beticola, Cladosporium herbarum, Fusarium culmorum,  
CC Fusarium graminearum or Phytophthora cinnamomi.  
XX  
SQ Sequence 44 BP; 10 A; 7 C; 20 G; 7 T; 0 other;  
  
Query Match 40.0%; Score 44; DB 20; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 aggtccgtgtgcaggcagatcaagatctgcaggaggggtgg 44  
|||||  
DB 1 aggtccgtgtgcaggcagatcaagatctgcaggaggggtgg 44  
|||||  
  
RESULT 5  
AAAX59772  
ID AAX59772 standard; cDNA; 98 BP.  
AC AAX59772;  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE cDNA encoding the signal peptide of the PR-1a gene of tobacco.  
XX  
KW Thanatine; fungal disease; bacterial disease; Cercospora beticola;  
KW Cladosporium herbarum; Fusarium culmorum; F. graminearum;  
KW Phytophthora cinnamomi; selection marker; plant transformation;  
KW herbicide resistance; PR-1a gene; tobacco; ss.  
XX  
OS Nicotiana tabacum.  
XX  
PN FR2770853-A1.  
XX

PD 14-MAY-1999.  
XX  
PF 07-NOV-1997; 97FR-0014263.  
XX  
PR 07-NOV-1997; 97FR-0014263.  
XX  
PA (RHON ) RHONE-POULENC AGROCHIMIE.  
XX  
PI Derose R, Freyssinet G, Hoffmann J;  
XX  
DR WPI; 1999-315645/27.  
DR P-PSDB; AAY15464.  
XX  
PT New nucleic acid encoding thanatine useful as a selection marker for  
XX transformation of plants  
XX  
PS Example 1; Page 14; 24pp; French.  
XX  
CC The specification describes a nucleic acid sequence containing the  
CC sequence that encodes thanatine. Plants transformed with this nucleic  
CC acid sequence are resistant to fungal and bacterial diseases,  
CC specifically those caused by Cercospora beticola, Cladosporium  
CC herbarum, Fusarium culmorum, F. graminearum and Phytophthora  
CC cinnamomi. The nucleic acid sequence may also be used as a selection  
CC marker for transformation of plants with other coding sequences,  
CC e.g. those that impart resistance to herbicides. The present sequence  
CC encodes the signal peptide of the PR-1a gene of tobacco, which was  
CC used to make fusion products of the invention.  
XX  
SQ Sequence 98 BP; 25 A; 23 C; 34 G; 16 T; 0 other;  
  
Query Match 31.8%; Score 35; DB 20; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 76 tgagtcctgcggaggcggaacgtgtgcagcgatccgg 110  
|||||  
DB 64 tgagtcctgcggaggcggaacgtgtgcagcgatccgg 98  
|||||  
  
RESULT 6  
AAZ45692  
ID AAZ45692 standard; DNA; 169 BP.  
XX  
AC AAZ45692;  
XX  
DT 06-APR-2000 (first entry)  
XX  
DE DNA encoding a heliomycin peptide.  
XX  
KW Heliomycin; polycysteine peptide; antifungal; antibacterial;  
KW fungal infection; plant protection; animal protection;  
KW transgenic plant; fungi; bacteria; Cercospora beticola;  
KW Cladosporium herbarum; Fusarium culmorum; F. oxysporum;  
KW Phytophthora cinnamomi; ss.  
XX  
OS Heliothis virescens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..135  
FT /tag= a  
FT /product= "heliomycin"  
XX  
PN FR2777568-A1.  
XX  
PD 22-OCT-1999.  
XX  
PF 15-APR-1998; 98FR-0004933.  
XX  
PR 15-APR-1998; 98FR-0004933.  
XX  
PA (RHON ) RHONE-POULENC AGROCHIMIE.

XX WPI; 2000-108532/10.  
 DR P-PSDB; AAY54375.  
 XX  
 PT New polycysteine peptides, designated heliomycin, with antifungal or  
 XX antibacterial activity, useful in medicine or plant protection -  
 XX  
 PS Claim 19; Page 31-32; 46pp; French.  
 XX  
 CC The present sequence encodes the heliomycin peptide. Helioimycin is a  
 CC polycysteine peptide with antifungal and antibacterial activity,  
 CC isolated from the lepidopteron *Heliothis virescens*. Helioimycin peptides  
 CC contain the sequence given in AAY54378. The heliomycin peptides are  
 CC used as pharmaceuticals for treating or preventing fungal infections  
 CC in humans and animals. They may also be used as antifungal agents for  
 CC plant protection. Nucleic acid encoding the heliomycin peptides is  
 CC used to generate transgenic plants that are resistant to some fungi  
 CC and bacteria (specifically *Cercospora beticola*, *Cladosporium herbarum*,  
 CC *Fusarium culmorum*, *F. oxysporum* and *Phytophthora cinnamoni*), and for  
 CC recombinant production of the peptides.  
 XX  
 SQ Sequence 169 BP; 33 A; 36 C; 61 G; 39 T; 0 other;  
 Query Match 30.9%; Score 34; DB 21; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 77 gagctcggcggagcagctgtcgcgagatccgg 110  
 |||||  
 Db 136 gagctcggcggagcagctgtcgcgagatccgg 169  
 |||||  
 RESULT 7  
 AAZ45693  
 ID AAZ45693 standard; DNA; 261 BP.  
 XX  
 AC AAZ45693;  
 XX  
 DT 06-APR-2000 (first entry)  
 XX  
 DE DNA encoding a fusion peptide of PR-1alpha signal peptide/heliomycin.  
 XX  
 KW PR-1alpha: heliomycin; polycysteine peptide; antifungal; antibacterial;  
 KW fungal infection; plant protection; animal protection; transgenic plant;  
 KW fungi; bacteria; *Cercospora beticola*; *Cladosporium herbarum*;  
 KW *Fusarium culmorum*; *F. oxysporum*; *Phytophthora cinnamoni*; ss.  
 XX  
 OS Chimeric - *Nicotiana sp.*  
 OS Chimeric - *Heliothis virescens*.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 3..227  
 FT /\*tag= a  
 FT sig\_peptide 1..92  
 FT /\*tag= b  
 FT /note= "these nucleotides encode the tobacco  
 FT PR-1alpha signal peptide"  
 FT mat\_peptide 93..224  
 FT /\*tag= c  
 FT /note= "these nucleotides encode heliomycin"  
 XX  
 PN FR2777568-A1.  
 XX  
 XX 22-OCT-1999.  
 PD  
 XX 15-APR-1998; 98FR-0004933.  
 XX  
 XX 15-APR-1998; 98FR-0004933.  
 XX  
 XX (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX  
 XX WPI; 2000-108532/10.  
 DR

DR P-PSDB; AAY54376.  
 XX  
 XX New polycysteine peptides, designated heliomycin, with antifungal or  
 PT antibacterial activity, useful in medicine or plant protection -  
 XX  
 XX Example 4; Page 32; 46pp; French.  
 PS  
 CC The present sequence encodes a fusion peptide of the tobacco  
 CC PR-1alpha signal peptide and heliomycin. The attachment of the  
 CC PR-1alpha sequence to the N-terminal aids secretion of the heliomycin  
 CC peptide. Helioimycin is a polycysteine peptide with antifungal and  
 CC antibacterial activity, isolated from the lepidopteron *Heliothis*  
 CC *virescens*. Helioimycin peptides contain the sequence given in  
 CC AAY54378. The heliomycin peptides are used as pharmaceuticals for  
 CC treating or preventing fungal infections in humans and animals. They  
 CC may also be used as antifungal agents for plant protection. Nucleic  
 CC acid encoding the heliomycin peptides is used to generate transgenic  
 CC plants that are resistant to some fungi and bacteria (specifically  
 CC *Cercospora beticola*, *Cladosporium herbarum*, *Fusarium culmorum*,  
 CC *F. oxysporum* and *Phytophthora cinnamoni*), and for recombinant production  
 CC of the peptides.  
 XX  
 SQ Sequence 261 BP; 39 A; 66 C; 74 G; 82 T; 0 other;  
 Query Match 30.9%; Score 34; DB 21; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 0.048;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 77 gagctcggcggagcagctgtcgcgagatccgg 110  
 |||||  
 Db 228 gagctcggcggagcagctgtcgcgagatccgg 261  
 |||||  
 RESULT 8  
 AAX59774  
 ID AAX59774 standard; cDNA; 197 BP.  
 XX  
 AC AAX59774;  
 XX  
 DT 26-JUL-1999 (first entry)  
 XX  
 DE cDNA encoding a thanatine fusion product of the invention.  
 XX  
 XX Thanatine: fungal disease; bacterial disease; *Cercospora beticola*;  
 KW *Cladosporium herbarum*; *Fusarium culmorum*; *F. graminearum*;  
 KW *Phytophthora cinnamoni*; selection marker; plant transformation;  
 KW herbicide resistance; PR-1a gene; tobacco; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX FR2770853-A1.  
 XX  
 PN 14-MAY-1999.  
 XX  
 PD 07-NOV-1997; 97FR-0014263.  
 XX  
 PF 07-NOV-1997; 97FR-0014263.  
 XX  
 PR (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX  
 PA Derose R, Freyssinet G, Hoffmann J;  
 XX  
 PI WPI: 1999-315645/27.  
 XX  
 DR P-PSDB; AAY13466.  
 DR  
 XX New nucleic acid encoding thanatine useful as a selection marker for  
 PT transformation of plants  
 XX  
 XX Claim 8; Page 14-15; 24pp; French.  
 PS  
 XX The specification describes a nucleic acid sequence containing the  
 CC sequence that encodes thanatine. Plants transformed with this nucleic  
 CC

CC acid sequence are resistant to fungal and bacterial diseases,  
 CC specifically those caused by *Cercospora beticola*, *Cladosporium*  
 CC *herbarum*, *Fusarium culmorum*, *F. graminearum* and *Phytophthora*  
 CC *cinnamomi*. The nucleic acid sequence may also be used as a selection  
 CC marker for transformation of plants with other coding sequences,  
 CC e.g. those that impart resistance to herbicides. The present sequence  
 CC encodes a thanatin fusion product of the invention, comprising the  
 CC signal peptide of the PR-1a gene of tobacco.  
 XX  
 SQ Sequence 197 BP; 32 A; 56 C; 49 G; 60 T; 0 other;

Query Match 30.0%; Score 33; DB 20; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 0.094;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 tgagctcgcgagcgacgtgtcgacggatcc 108  
 |||||  
 Db 165 tgagctcgcgagcgacgtgtcgacggatcc 197

RESULT 9  
 AAV57926  
 ID AAV57926 standard; DNA; 235033 BP.  
 AC AAV57926;  
 XX

DT 23-DEC-1998 (first entry)  
 XX

DE Hereditary haemochromatosis subregion from an unaffected individual.  
 XX  
 KW Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;  
 diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;  
 BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;  
 KW type 1 sodium transport gene; ss.  
 XX  
 OS Homo sapiens.  
 XX

PN WO9814466-A1.  
 XX  
 PD 09-APR-1998.  
 XX

PF 30-SEP-1997; 97WO-US17658.  
 XX

PR 07-MAY-1997; 97US-0852495.  
 XX

PR 01-OCT-1996; 96US-0724394.  
 XX

PA (PROG-) PROGENITOR INC.  
 XX

PI Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;  
 PI Tsuchihashi Z, Wolff RK;  
 XX

DR WPI; 1998-240014/21.  
 XX

XX Hereditary haemochromatosis gene products - used to develop products  
 PT for the diagnosis and treatment of hereditary disorders in iron  
 PT metabolism  
 XX

XX Example 2; Fig 8; 209pp; English.  
 XX

CC The present invention describes hereditary haemochromatosis gene  
 CC products from the human haemochromatosis gene. The present sequence  
 CC represents a hereditary haemochromatosis subregion from an individual  
 CC unaffected by hereditary haemochromatosis (HH). Also described is a  
 CC method to determine the presence or absence of the common hereditary  
 CC haemochromatosis (HFE) gene mutation in an individual comprising:  
 CC (a) providing DNA or RNA from the individual; and (b) assessing the  
 CC DNA or RNA for the presence or absence of a haplotype or genotype where  
 CC the presence or absence of the haplotype genotype indicates the likely  
 CC presence of the HFE gene mutation in the genome of the individual. The  
 CC HFE gene sequences from the present invention can be used to develop  
 CC products for use in the diagnosis and treatment of HFE. The present  
 CC invention also describes BTF genes, which are homologues of the milk  
 CC

CC protein butyrophilin (BT), and can be used in the production of agonists  
 CC and antagonists of BT function. Also described are: (1) a RoRet gene  
 CC which can be used to develop products for the study, diagnosis and  
 CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes  
 CC which are homologues of a type 1 sodium transport gene, and can  
 CC similarly be used for hypophosphatemia.  
 XX

SQ Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;

Query Match 27.5%; Score 30.2; DB 19; Length 235033;  
 Best Local Similarity 69.5%; Pred. No. 5.1;  
 Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 agtccgtgtgcaggcagatcatctgcaggagggaggtgtgtgtctactacaagt 59  
 |||||  
 Db 192069 agaccatgagcttgagagcatgaagtacaggaggggtgtttcaataaatctg 192127

RESULT 10  
 AAV57903  
 ID AAV57903 standard; DNA; 237326 BP.  
 XX  
 AC AAV57903;  
 XX

DT 21-DEC-1998 (first entry)  
 XX

DE Hereditary haemochromatosis subregion from an HH affected individual.  
 XX

KW Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;  
 diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;  
 BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;  
 KW type 1 sodium transport gene; ss.  
 XX  
 OS Homo sapiens.  
 XX

PN WO9814466-A1.  
 XX  
 PD 09-APR-1998.  
 XX

PF 30-SEP-1997; 97WO-US17658.  
 XX

PR 07-MAY-1997; 97US-0852495.  
 XX

PR 01-OCT-1996; 96US-0724394.  
 XX

PA (PROG-) PROGENITOR INC.  
 XX

PI Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;  
 PI Tsuchihashi Z, Wolff RK;  
 XX

DR WPI; 1998-240014/21.  
 XX

XX Hereditary haemochromatosis gene products - used to develop products  
 PT for the diagnosis and treatment of hereditary disorders in iron  
 PT metabolism  
 XX

XX Claim 1; Fig 9; 209pp; English.  
 XX

CC The present invention describes hereditary haemochromatosis gene  
 CC products from the human haemochromatosis gene. The present sequence  
 CC represents a hereditary haemochromatosis subregion from an hereditary  
 CC haemochromatosis (HH) affected individual. Also described is a  
 CC method to determine the presence or absence of the common hereditary  
 CC haemochromatosis (HFE) gene mutation in an individual comprising:  
 CC (a) providing DNA or RNA from the individual; and (b) assessing the  
 CC DNA or RNA for the presence or absence of a haplotype or genotype where  
 CC the presence or absence of the haplotype genotype indicates the likely  
 CC presence of the HFE gene mutation in the genome of the individual. The  
 CC HFE gene sequences from the present invention can be used to develop  
 CC products for use in the diagnosis and treatment of HFE. The present  
 CC invention also describes BTF genes, which are homologues of the milk  
 CC protein butyrophilin (BT), and can be used in the production of agonists  
 CC and antagonists of BT function. Also described are: (1) a RoRet gene  
 CC



The present sequence encodes mouse Asx (additional sex comb) protein. Over- or under-expression of Asx, or expression of a variant Asx, is indicative of cancer, especially colorectal adenocarcinoma, melanoma, lymphoma or leukaemia. Diagnosis (or monitoring of disease) is done using DNA encoding Asx-based probes; amplification with DNA encoding Asx-derived primers; hybridisation with branched DNA (bDNA) probes that are specific for DNA encoding Asx; using Ab or by quantitation of RNA. Modulators that increase transcription of Asx are potentially useful as antineoplastic agents, e.g. for treating cancers specified above or other proliferative disorders such as stenosis, benign prostatic hypertrophy, retinopathy, psoriasis, arthritis and premalignant lesions. These conditions can also be treated with DNA encoding Asx in standard gene therapy processes. The Asx gene promoter is useful for tissue-

Db 76 gggggccctgctgagcgcgctcagccgctcggttcg 111

Search completed: April 2, 2002, 21:34:19  
Job time: 4391 sec

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Matches 53;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;

[illegible]

RESULT 15  
AAI49861  
ID AAI49861 standard; DNA; 193 BP.  
XX  
AC  
AAI49861;  
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DT  
17-OCT-2001 (first entry)  
XX  
DE  
Probe #18547 used to measure gene expression in human placenta sample.  
XX  
DE  
Probe; microarray; human; placenta; antenatal diagnosis;  
XX  
KW  
genetic disorder; ss.  
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OS  
Homo sapiens.  
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PN  
WO200157272-A2.  
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09-AUG-2001.  
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30-JAN-2001; 2001WO-US00663.  
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PF  
04-FEB-2000; 2000US-0180312.  
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PR  
26-MAY-2000; 2000US-0207456.  
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PR  
30-JUN-2000; 2000US-0608408.  
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PR  
03-AUG-2000; 2000US-0632366.  
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21-SEP-2000; 2000US-0234687.  
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PR  
27-SEP-2000; 2000US-0236359.  
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PR  
04-OCT-2000; 2000GB-0024263.  
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PA  
(MOLE-) MOLECULAR DYNAMICS INC.  
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PI  
Penn SG, Hanzel DK, Chen W, Rank DR;  
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WPI; 2001-488897/53.  
XX  
XX  
Human genome-derived single exon nucleic acid probes useful for  
PT  
analyzing gene expression in human placenta -  
PT  
XX  
PS  
Claim 25; SEQ ID No 18547; 654pp; English.  
XX  
CC  
The present invention relates to single exon nucleic acid probes (SENPs).  
CC  
The present sequence is one such probe. The probes are useful for  
CC  
producing a microarray for predicting, measuring and displaying gene  
CC  
expression in samples derived from human placenta. The probes are useful  
CC  
for antenatal diagnosis of human genetic disorders.  
XX  
XX  
Sequence 193 BP; 19 A; 80 C; 70 G; 24 T; 0 other;  
SQ

	Query Match	24.7%	Score 27.2;	DB 22;	Length 193;
	Best Local Similarity	55.2%;	Prod. No. 7.5;		
	Matches 53;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;
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Db	16	ccgccccagaccgaggccgagggtgcgtgagcagagcgcagagctgcgcgccacot	75		
Qy	65	acaggccatctagctcggcgaggcgaactgtctg	100		